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FIGURE 1

FIG. 1a

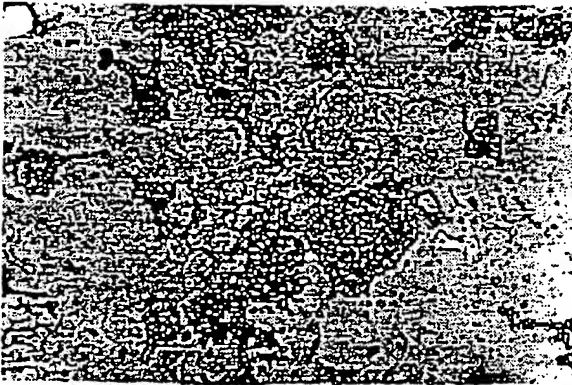


FIG. 1b

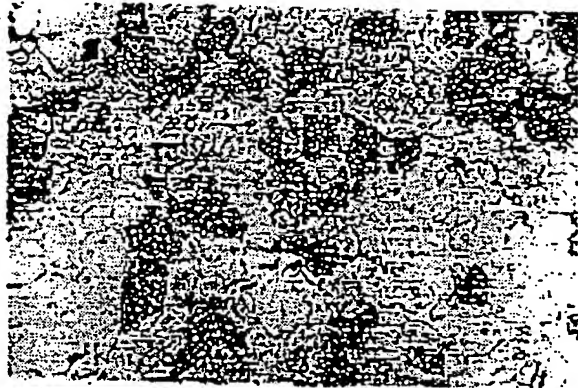


FIG. 1c

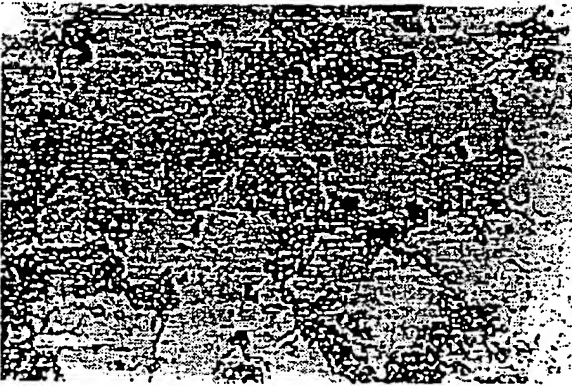


FIG. 1d



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FIGURE 2

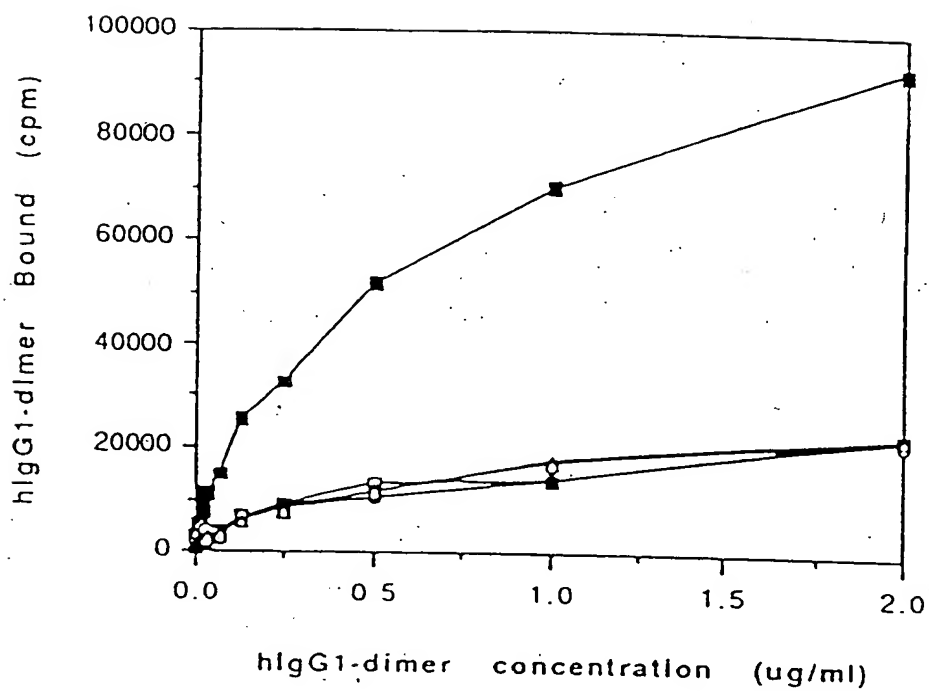


FIGURE 3

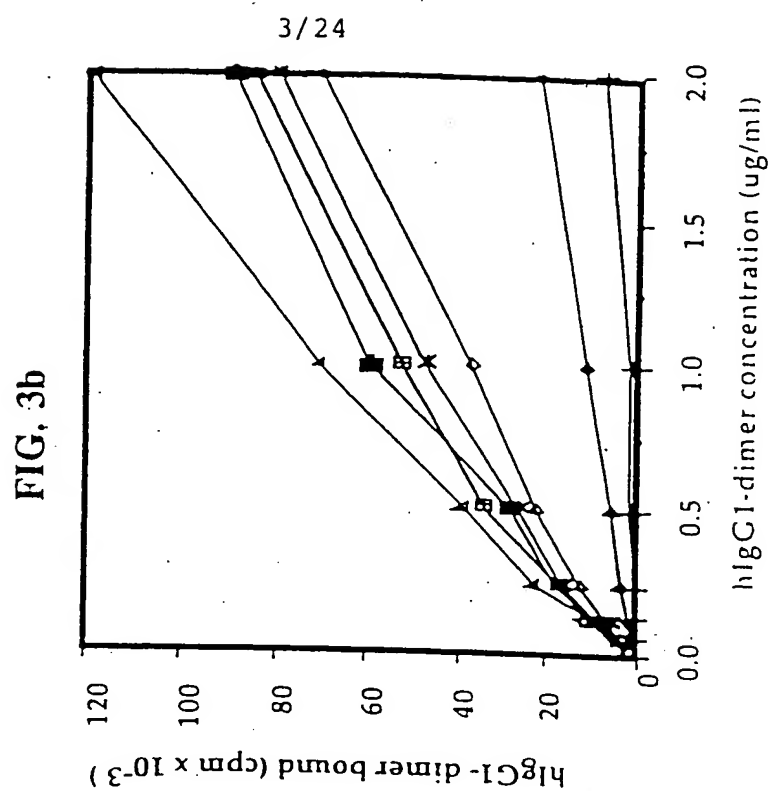
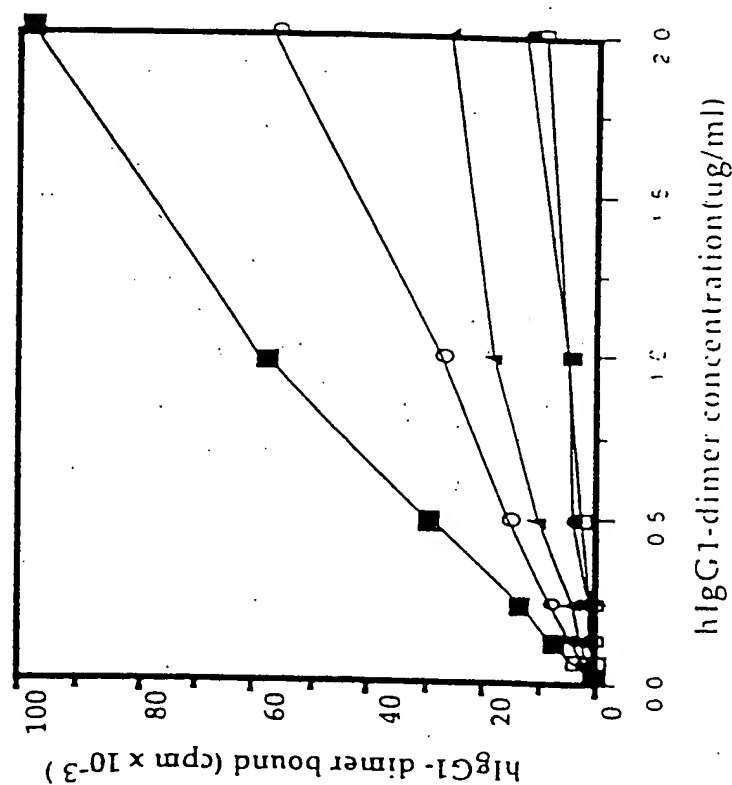


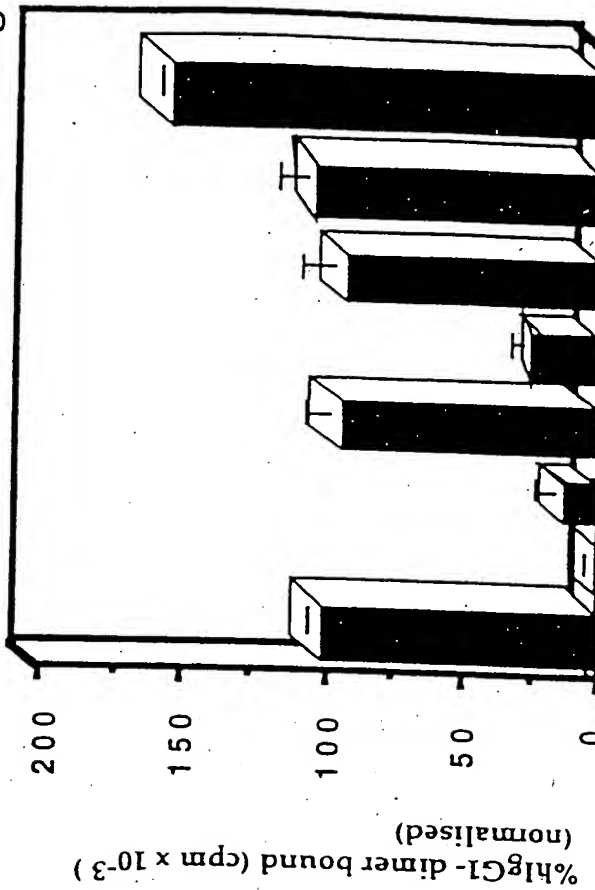
FIG. 3a



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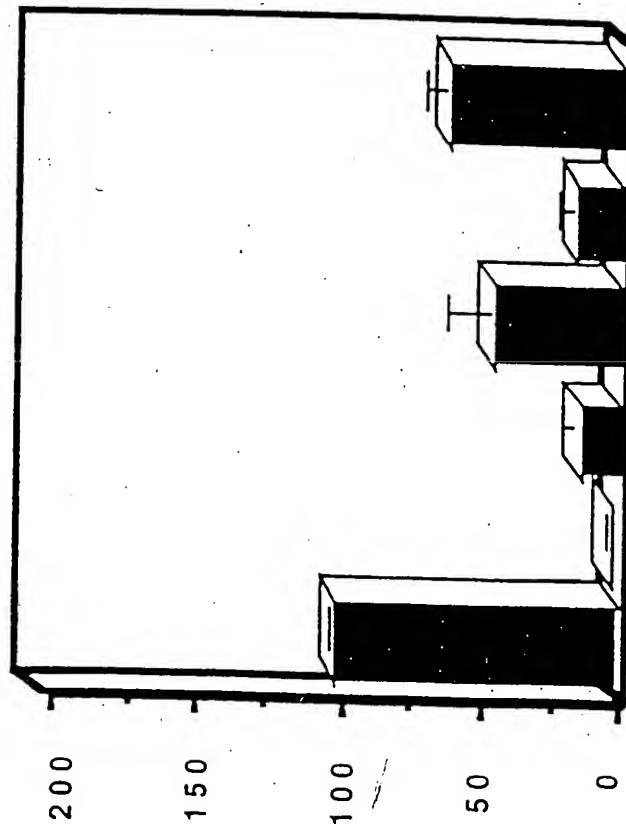
FIGURE 3 CONT'D

FIG. 3d



WT FcγRII PHE SER HIS LEU ASP PRO
FcγRII 129 130 131 132 133 134

FIG. 3c



WT FcγRII LYS PRO LEU VAL
FcγRII 113 114 115 116

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FIGURE 4

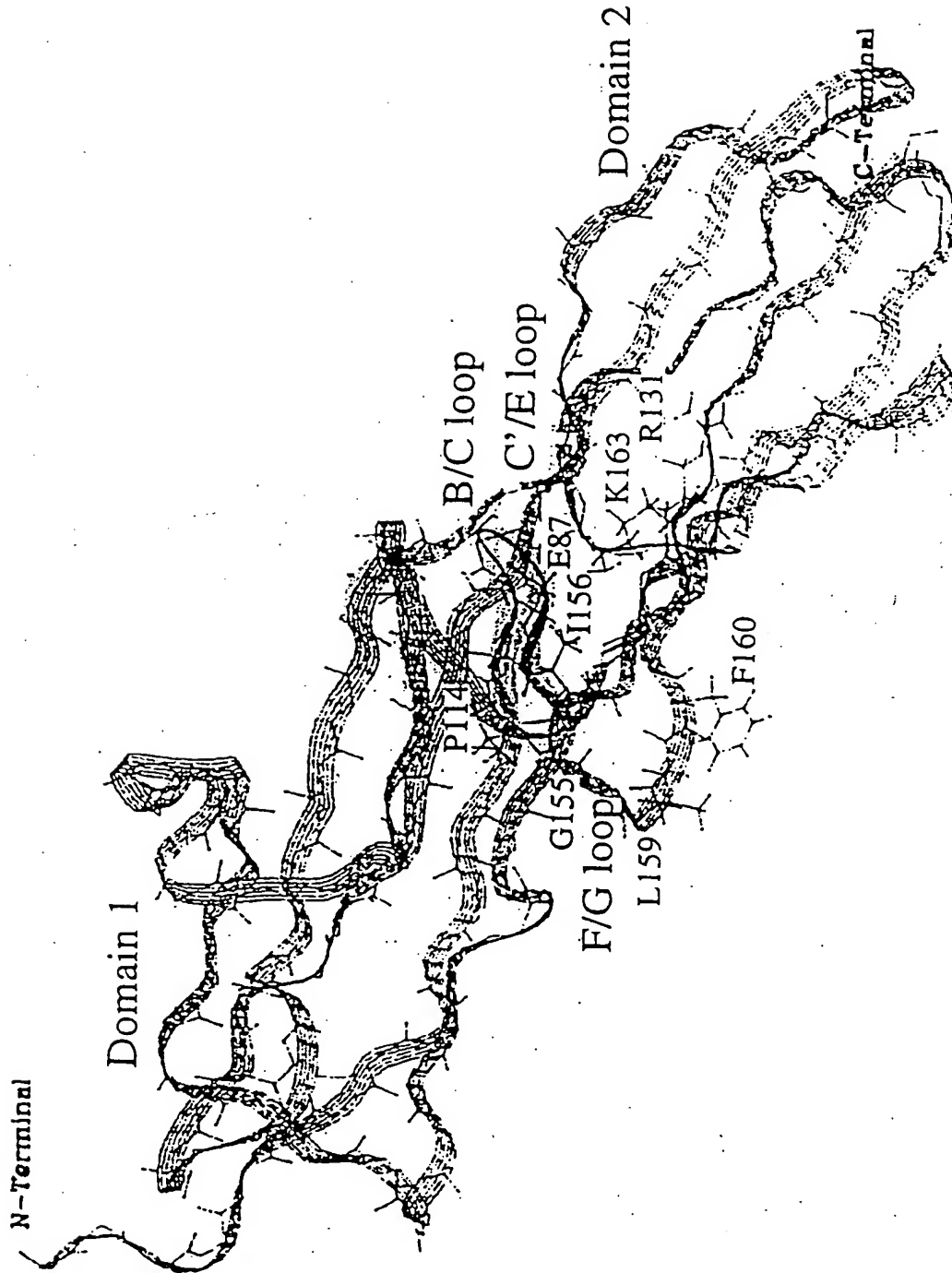


FIGURE 5

huFcRIa chain C'-E, F-G loop Ala mutant oligo nucleotides

F-G loop

5

e154 (Lys) \otimes Ala EFG-01 + EFG-02

EFG-01: 5' CTGTACGGGCGCAGTGTGGCAGC 3'

EFG-02: 5' GCTGCCACACTGCGCCCGTACAG 3'

10 e155 (Val) \otimes Ala EFG-03 + EFG-04

EFG-03: 5' GTACCGGCAAAGCATGGCAGCTGG 3'

EFG-04: 5' CCAGCTGCCATGCTTTGCCCCGTAC 3'

e156 (Trp) \otimes Ala EFG-05 + EFG-06

15 EFG-05: 5' GGGCAAAGTGGCACAGCTGGAC 3'

EFG-06: 5' GTCCAGCTGTGCCACTTTGCCC 3'

e157 (Gln) \otimes Ala EFG-07 + EFG-08

EFG-07: 5' GCAAAGTGTGGGCACTGGACTATG 3'

20 EFG-08: 5' CATAGTCCAGTGCCACACTTTGC 3'

e158 (Leu) \otimes Ala EFG-09 + EFG-10

EFG-09: 5' GTGTGGCAGGCAGACTATGAGTC 3'

EGG-10: 5' GACTCATAGTCTGCCTGCCACAC 3'

25

e159 (Asp) \otimes Ala EFG-11 + EFG-12

EFG-11: 5' GTGGCAGCTGGCATATGAGTCTG 3'

EFG-12: 5' CAGACTCATATGCCAGCTGCCAC 3'

30 e160 (Tyr) \otimes Ala EFG-13 + EFG-14

EFG-13: 5' GCAGCTGGACGCAGAGTCTGAGC 3'

EFG-14: 5' GCTCAGACTCTGCGTCCAGCTGC 3'

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Figure 5 cont.

e161 (Glu) * Ala

EFG-07+EFG-08

EFG-15: 5' GCTGGACTATGCATCTGAGCCCC 3'

EFG-16: 5' GGGGCTCAGATGCATAGTCCAGC 3'

5 C'-E loop

e129 (Tyr) * Ala

EBS-01+EBS-02

EBS-01: 5' GCTCTCAAGGCATGGTATGAGAAC 3'

EBS-02: 5' GTTCTCATACCATGCCTTGAGAGC 3'

10

e130 (Trp) * Ala

EBS-03+EBS-04

EBS-03: 5' CTCAAGTACGCATATGAGAACCAC 3'

EBS-04: 5' GTGGTTCTCATATGCGTACTTGAG 3'

15 e131 (Tyr) * Ala

EBS-01+EBS-02

EBS-05: 5' CAAGTACTGGGCAGAGAACCAC 3'

EBS-06: 5' GTGGTTCTCTGCCAGTACTTG 3'

e132 (Glu) * Ala

EBS-07+EBS-08

20 EBS-07: 5' GTACTGGTATGCAAACCACAACATC 3'

EBS-08: 5' GATGTTGTGGTTTGCATACCAGTAC 3'

e133 (Asn) * Ala

EBS-09+EBS-10

EBS-09: 5' CTGGTATGAGGCACACAACATCTCC 3'

25 EBS-10: 5' GGAGATGTTGTGTGCCTCATACCAG 3'

e134 (His) * Ala

EBS-11+EBS-12

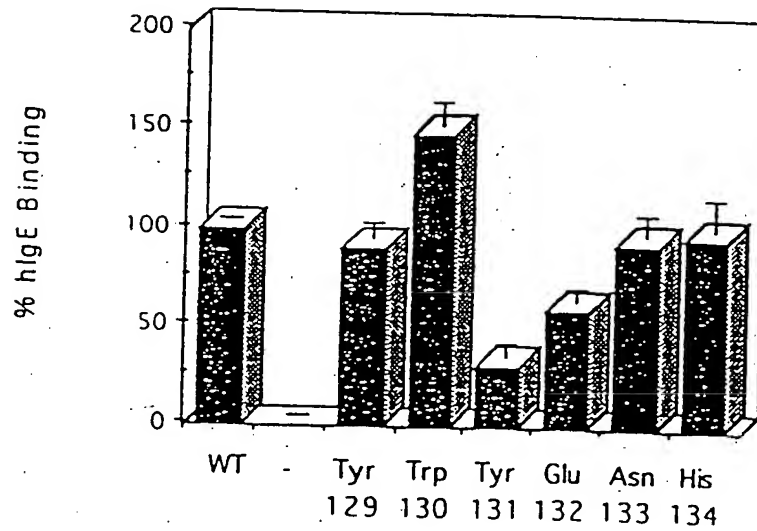
EBS-11: 5' GGTATGAGAACGCAAACATCTCCATTAC 3'

EBS-12: 5' GTAATGGAGATGTTTGC GTTCTCATACC 3'

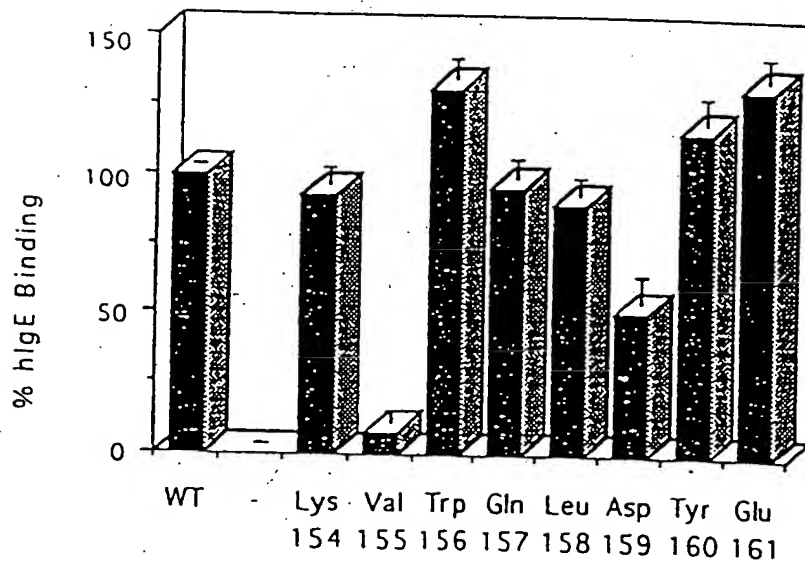
30

FIGURE 6

Effect of mutation of the IgE receptor (FcεRI) on the binding of IgE
C'-E LOOP



F-G LOOP



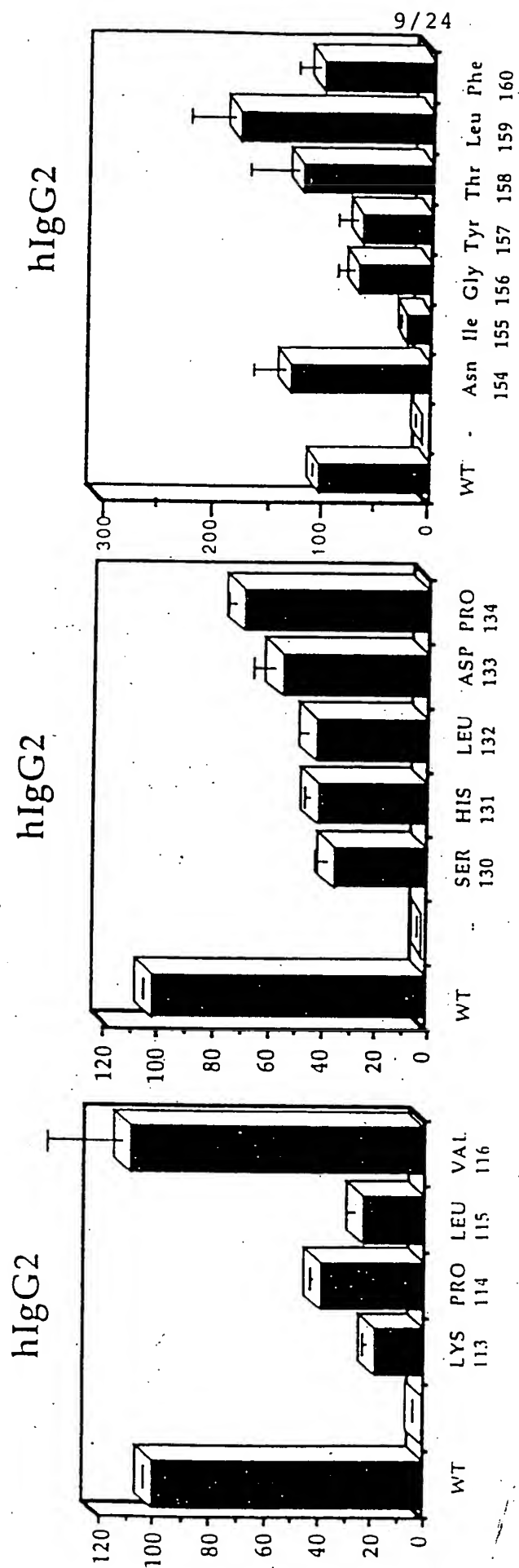


FIGURE 7

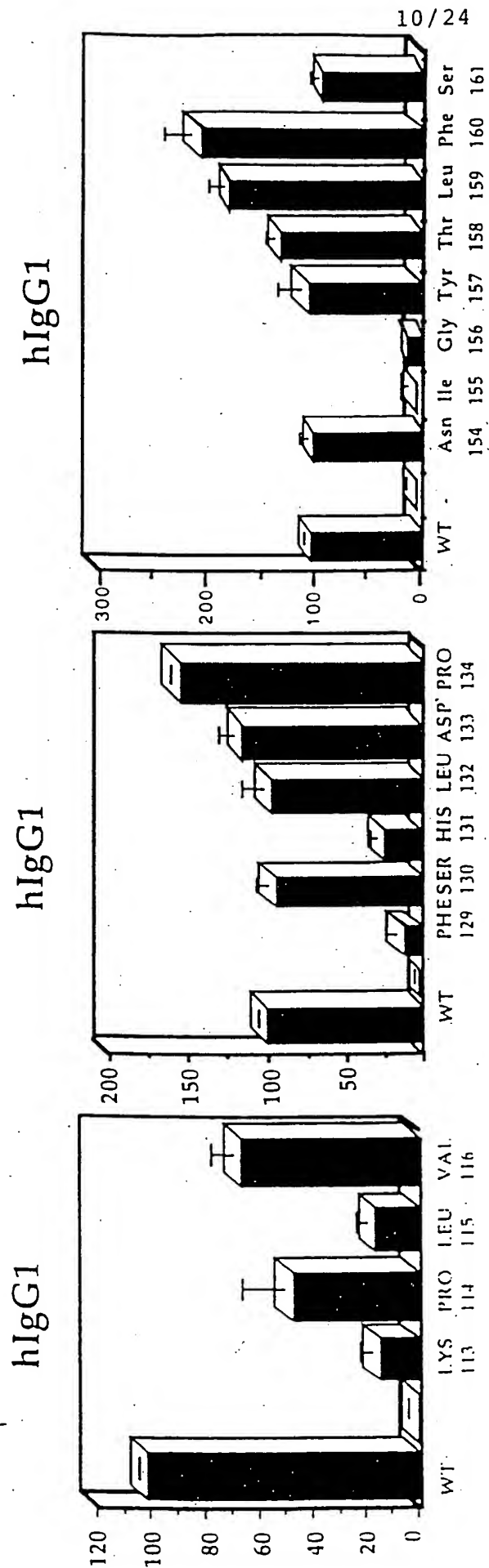
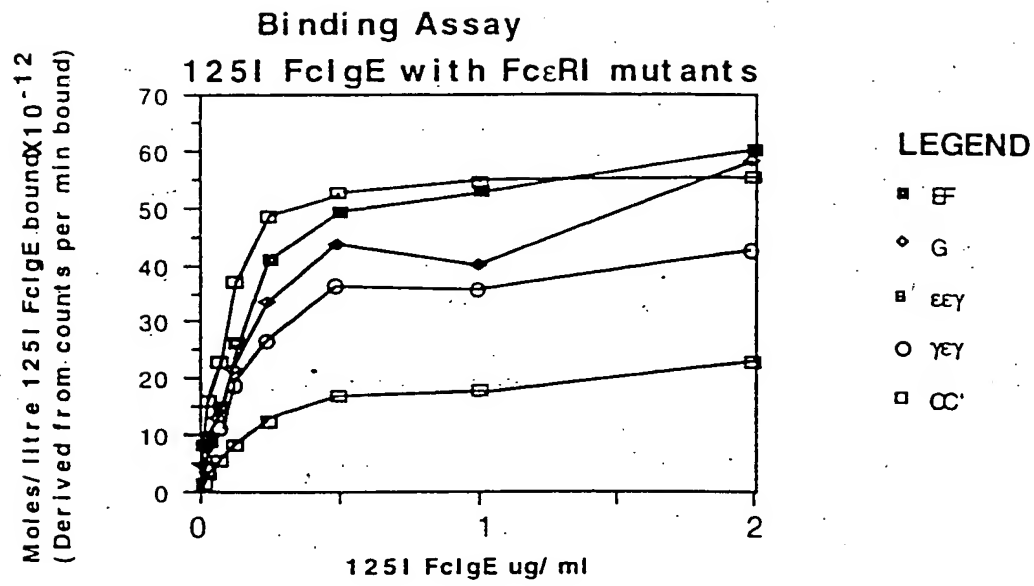


FIGURE 7 CONT'D...

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FIGURE 8



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FIGURE 9

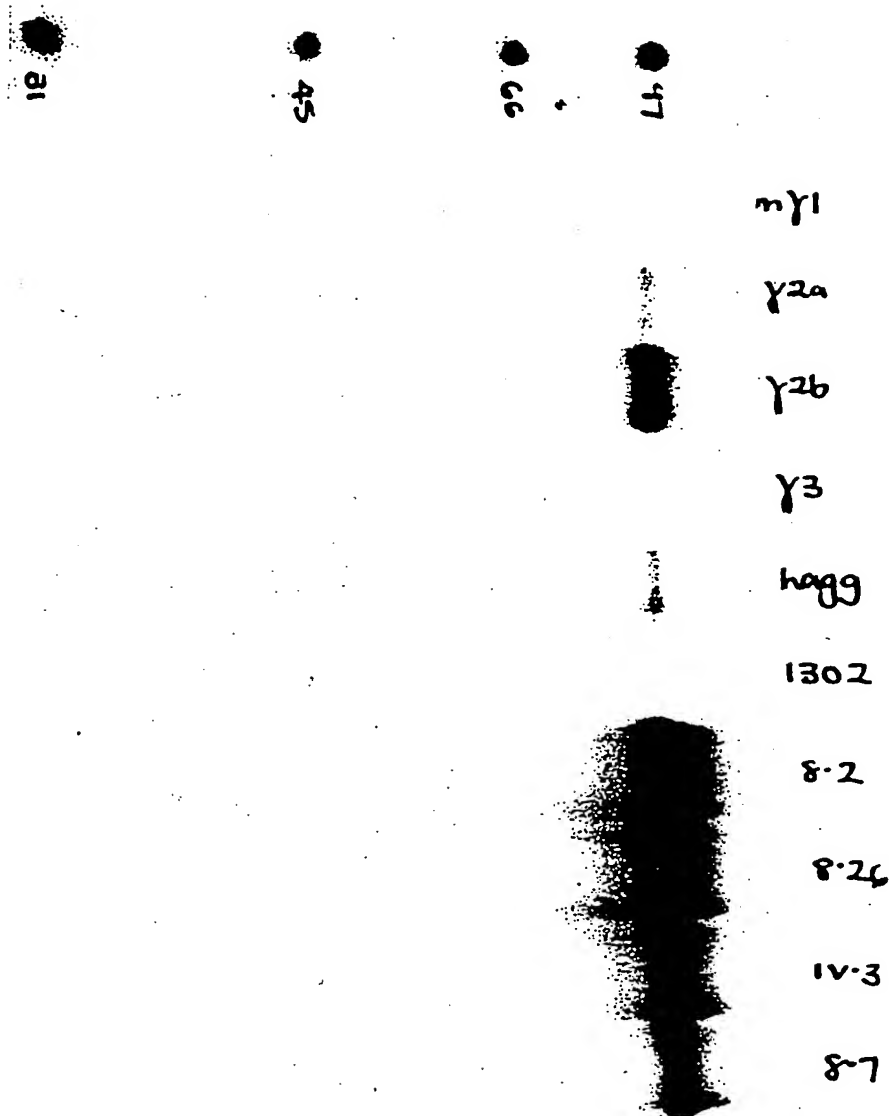


FIGURE 10

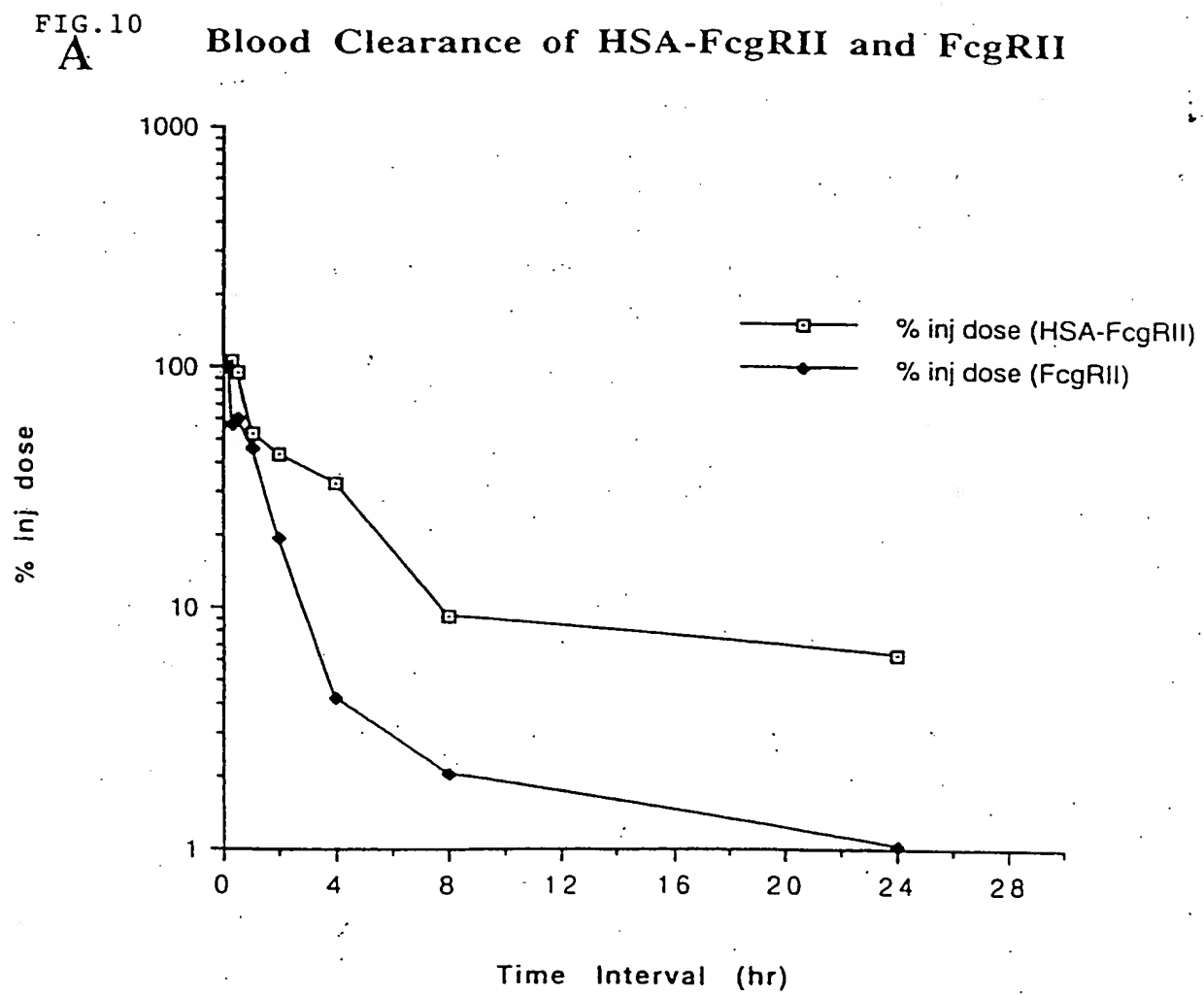


FIGURE 10 CONT'D..

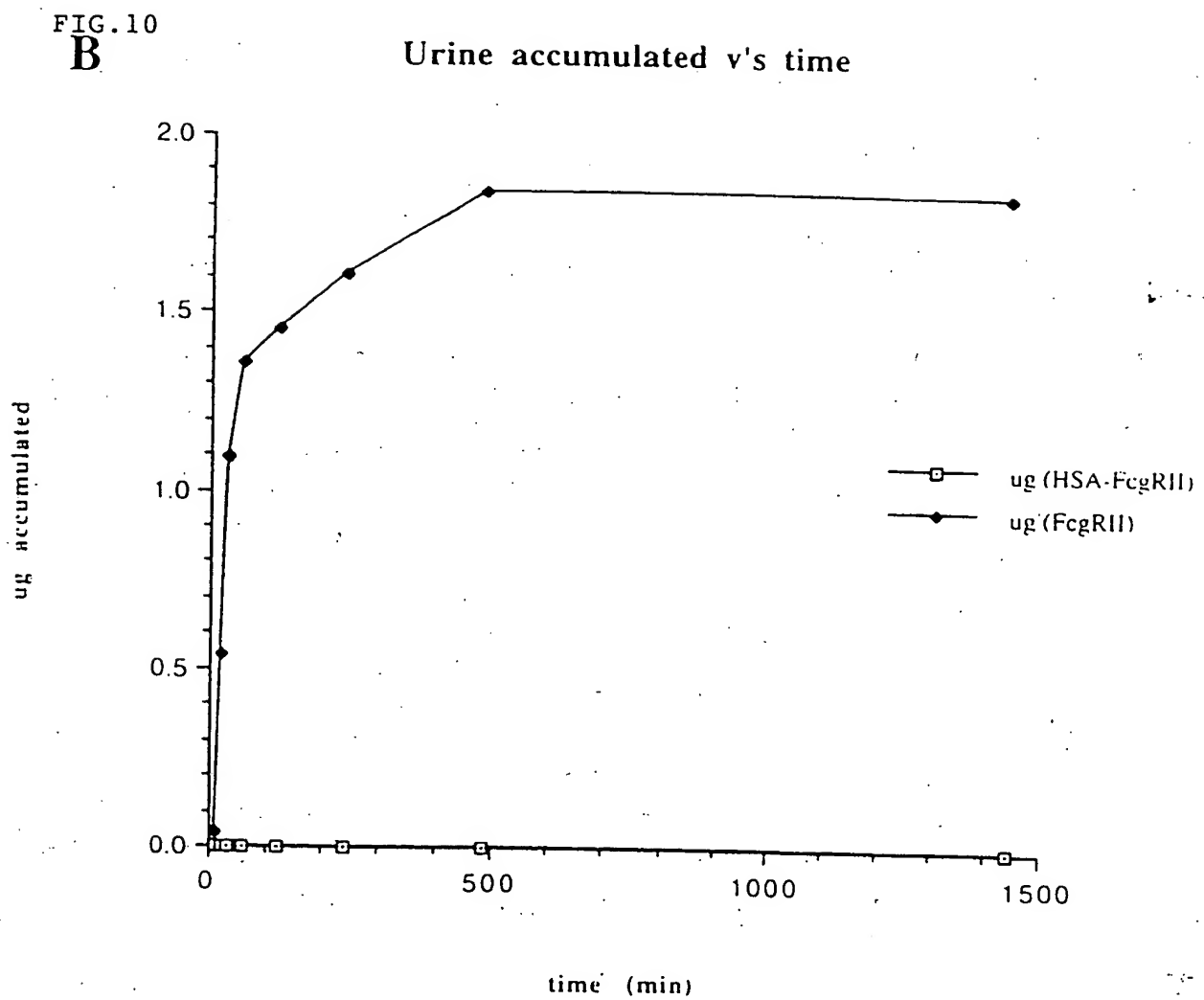


FIGURE 11

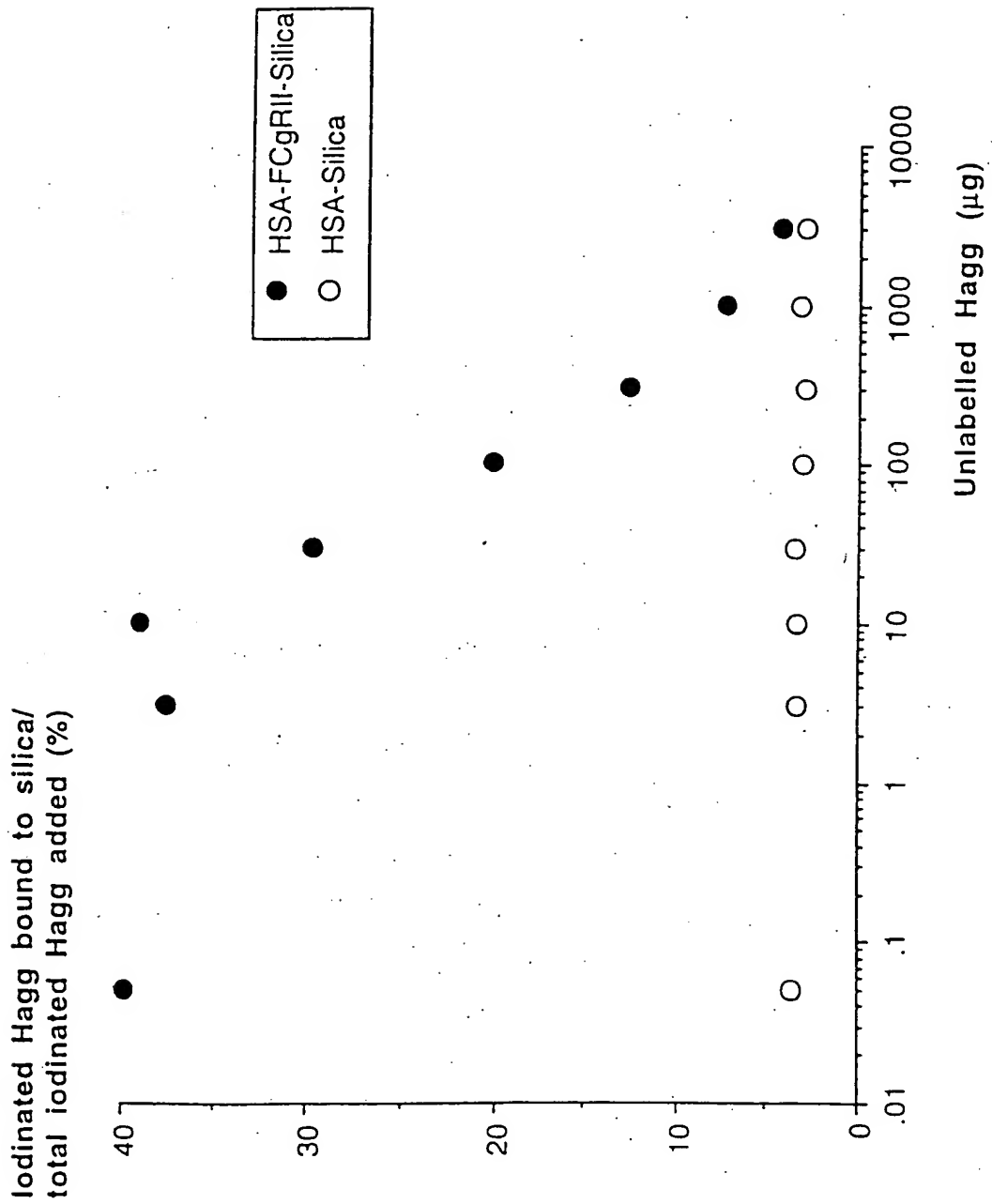


FIGURE 12

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1/1	31/11
GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG	TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA
asp ala his lys ser glu val ala his arg	phe lys asp leu gly glu glu asn phe lys
61/21	91/31
GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT	CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA
ala leu val leu ile ala phe ala gln tyr	leu gln gln cys pro phe glu asp his val
121/41	151/51
AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA	AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA
lys leu val asn glu val thr glu phe ala	lys thr cys val ala asp glu ser ala glu
181/61	211/71
AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT	GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT
asn cys asp lys ser leu his thr leu phe	gly asp lys leu cys thr val ala thr leu
241/81	271/91
CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC	TGT GCA AAA CAA GAA CCT GAG AGA AAT GAA
arg glu thr tyr gly glu met ala asp cys	cys ala lys gln glu pro glu arg asn glu
301/101	331/111
TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA	AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT
cys phe leu gln his lys asp asp asn pro	asn leu pro arg leu val arg pro glu val
361/121	391/131
GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT	GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT
asp val met cys thr ala phe his asp asn	glu glu thr phe leu lys lys tyr leu tyr
421/141	451/151
GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT	GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG
glu ile ala arg arg his pro tyr phe tyr	ala pro glu leu leu phe phe ala lys arg
481/161	511/171
TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA	GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA
tyr lys ala ala phe thr glu cys cys gln	ala ala asp lys ala ala cys leu leu pro
541/181	571/191
AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG	GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT
lys leu asp glu leu arg asp glu gly lys	ala ser ser ala lys gln arg leu lys cys
601/201	631/211
GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT	TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC
ala ser leu gln lys phe gly glu arg ala	phe lys ala trp ala val ala arg leu ser
661/221	691/231
CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA	GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA
gln arg phe pro lys ala glu phe ala glu	val ser lys leu val thr asp leu thr lys
721/241	751/251
GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG	CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT
val his thr glu cys cys his gly asp leu	leu glu cys ala asp asp arg ala asp leu
781/261	811/271
GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG	ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA
ala lys tyr ile cys glu asn gln asp ser	ile ser ser lys leu lys glu cys cys glu
841/281	871/291
AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT	GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT
lys pro leu leu glu lys ser his cys ile	ala glu val glu asn asp glu met pro ala
901/301	931/311
GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT	GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT
asp leu pro ser leu ala ala asp phe val	glu ser lys asp val cys lys asn tyr ala
961/321	991/331
GAG GCA AAG GAT GTC TTC CTG GGC ATG TTT	TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT
glu ala lys asp val phe leu gly met phe	leu tyr glu tyr ala arg arg his pro asp
1021/341	1051/351
TAC TCT GTC GTG CTG CTG CTG AGA CTT GCC	AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC
tyr ser val val leu leu leu arg leu ala	lys thr tyr glu thr thr leu glu lys cys
1081/361	1111/371
TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT	GCC AAA GTG TTC GAT GAA TTT AAA CCT CTT
cys ala ala ala asp pro his glu cys tyr	ala lys val phe asp glu phe lys pro leu
1141/381	1171/391
GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA	AAT TGT GAG CTT TTT GAG CAG CTT GGA GAG
val glu glu pro gln asn leu ile lys gln	asn cys glu leu phe glu gln leu gly glu
1201/401	1231/411
TAC AAA TTC CAG AAT GCG CTA TTA GTT CGT	TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT
tyr lys phe gln asn ala leu leu val arg	tyr thr lys lys val pro gln val ser thr
1261/421	1291/431

FIGURE 12 CONT'D...

CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT
 pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his
 1321/441
 CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA
 pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu
 1381/461
 TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT GAC AGA GTC ACA AAA TGC TGC ACA GAA TCC
 cys val leu his glu lys thr pro val ser asp arg val thr lys cys cys thr glu ser
 1441/481
 TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA
 leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys
 1501/501
 GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG
 glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu
 1561/521
 AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA
 arg gln ile lys lys gln thr ala leu val glu leu val lys his lys pro lys ala thr
 1621/541
 AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCA GCT TTT GTA GAG AAG TGC TGC AAG
 lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys
 1681/561
 GCT GAC GAT AAG AAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA
 ala asp asp lys lys thr cys phe ala glu glu gly lys lys leu val ala ala ser gln
 1741/581
 GCT GCC TTA GGC GCT CCC CCA AAG GCT GTG CTG AAA CTT GAG CCC CCG TGG ATC AAC GTG
 ala ala leu gly ala pro pro lys ala val leu lys leu glu pro pro trp ile asn val
 1801/601
 CTC CAG GAG GAC TCT GTG ACT CTG ACA TGC CAG GGG GCT CGC AGC CCT GAG AGC GAC TCC
 leu gln glu asp ser val thr leu thr cys gln gly ala arg ser pro glu ser asp ser
 1861/621
 ATT CAG TGG TTC CAC AAT GGG AAT CTC ATT CCC ACC CAC ACg CAG CCC AGC TAC AGG TTC
 ile gln trp phe his asn gly asn leu ile pro thr his thr gln pro ser tyr arg phe
 1921/641
 AAG GCC AAC AAC AAT GAC AGC GGG GAG TAC ACG TGC CAG ACT GGC CAG ACC AGC CTC AGC
 lys ala asn asn asn asp ser gly glu tyr thr cys gln thr gly gln thr ser leu ser
 1981/661
 GAC CCT GTG CAT CTG ACT GTG CTT TCC GAA TGG CTG GTG CTC CAG ACC CCT CAC CTG GAG
 asp pro val his leu thr val leu ser glu trp leu val leu gln thr pro his leu glu
 2041/681
 TTC CAG GAG GGA GAA ACC ATC ATG CTG AGG TGC CAC AGC TGG AAG GAC AAG CCT CTG GTC
 phe gln glu gly glu thr ile met leu arg cys his ser trp lys asp lys pro leu val
 2101/701
 AAG GTC ACA TTC TTC CAG AAT GGA AAA TCC CAG AAA TTC TCC CAT TTG GAT CCC ACC TTC
 lys val thr phe phe gln asn gly lys ser gln lys phe ser his leu asp pro thr phe
 2161/721
 TCC ATC CCA CAA GCA AAC CAC AGT CAC AGT GGT GAT TAC CAC TGC ACA GGA AAC ATA GGC
 ser ile pro gln ala asn his ser his ser gly asp tyr his cys thr gly asn ile gly
 2221/741
 TAC ACG CTG TTC TCA TCC AAG CCT GTG ACC ATC ACT GTC CAA TAG
 tyr thr leu phe ser ser lys pro val thr ile thr val gln AMB

FIGURE 13

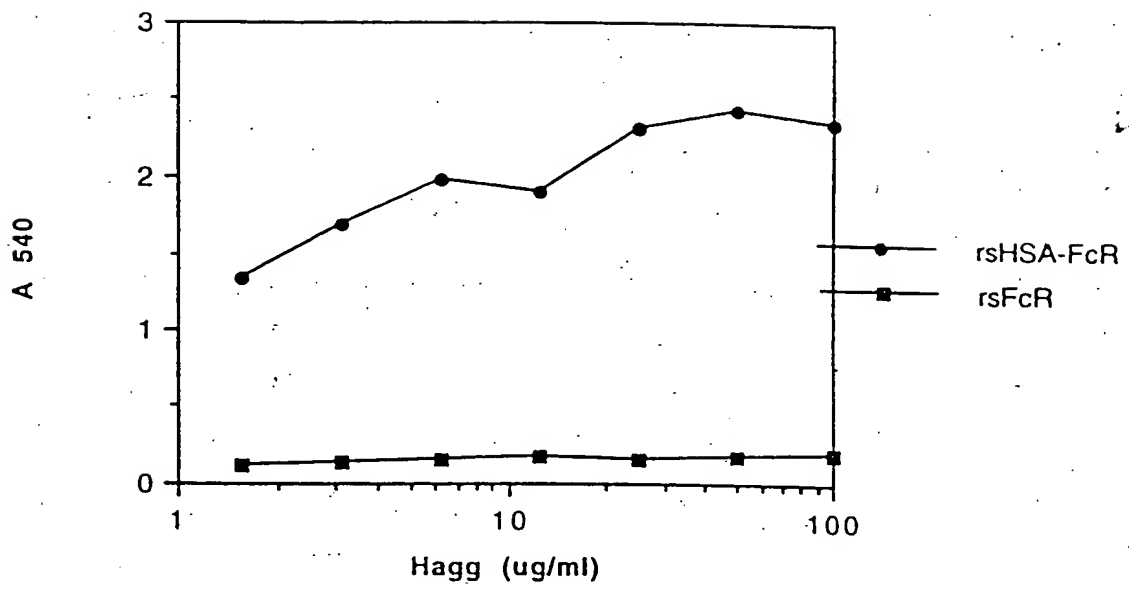


FIGURE 14

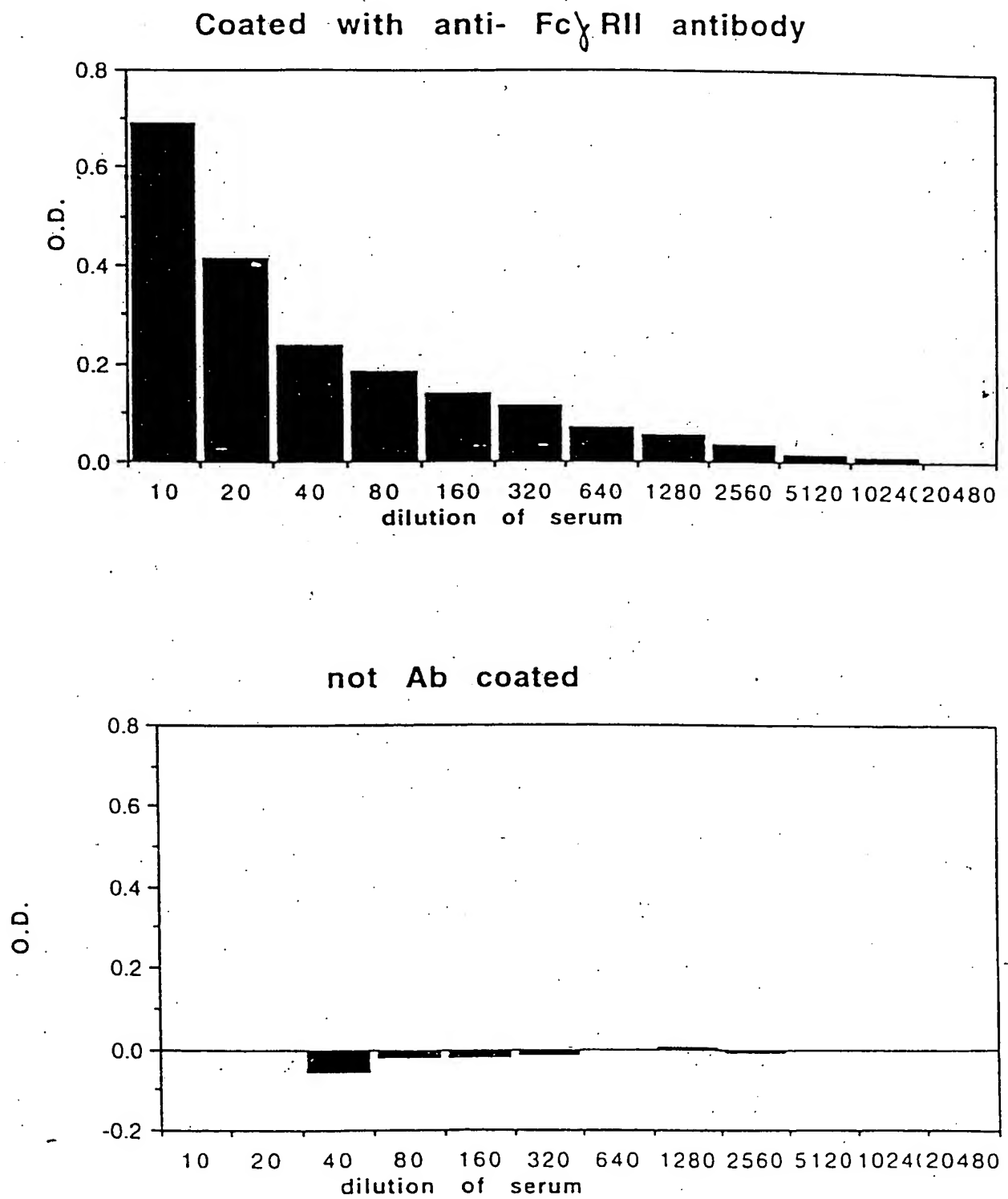


FIGURE 15

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Depletion of Heat aggregated Ig (Hagg) using FcγRII-HSA silica

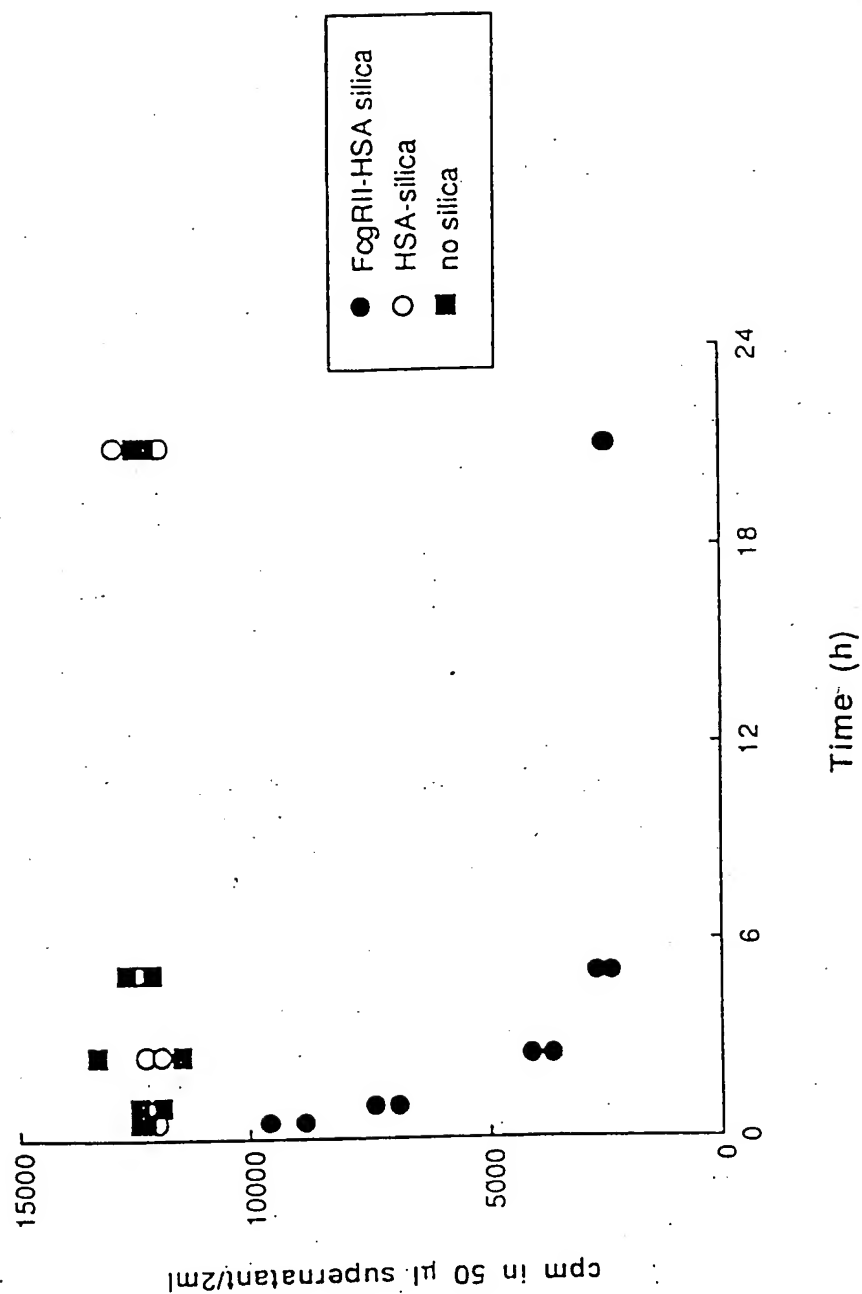


FIGURE 16

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No depletion of monomeric Ig using FcγRII-HSA silica

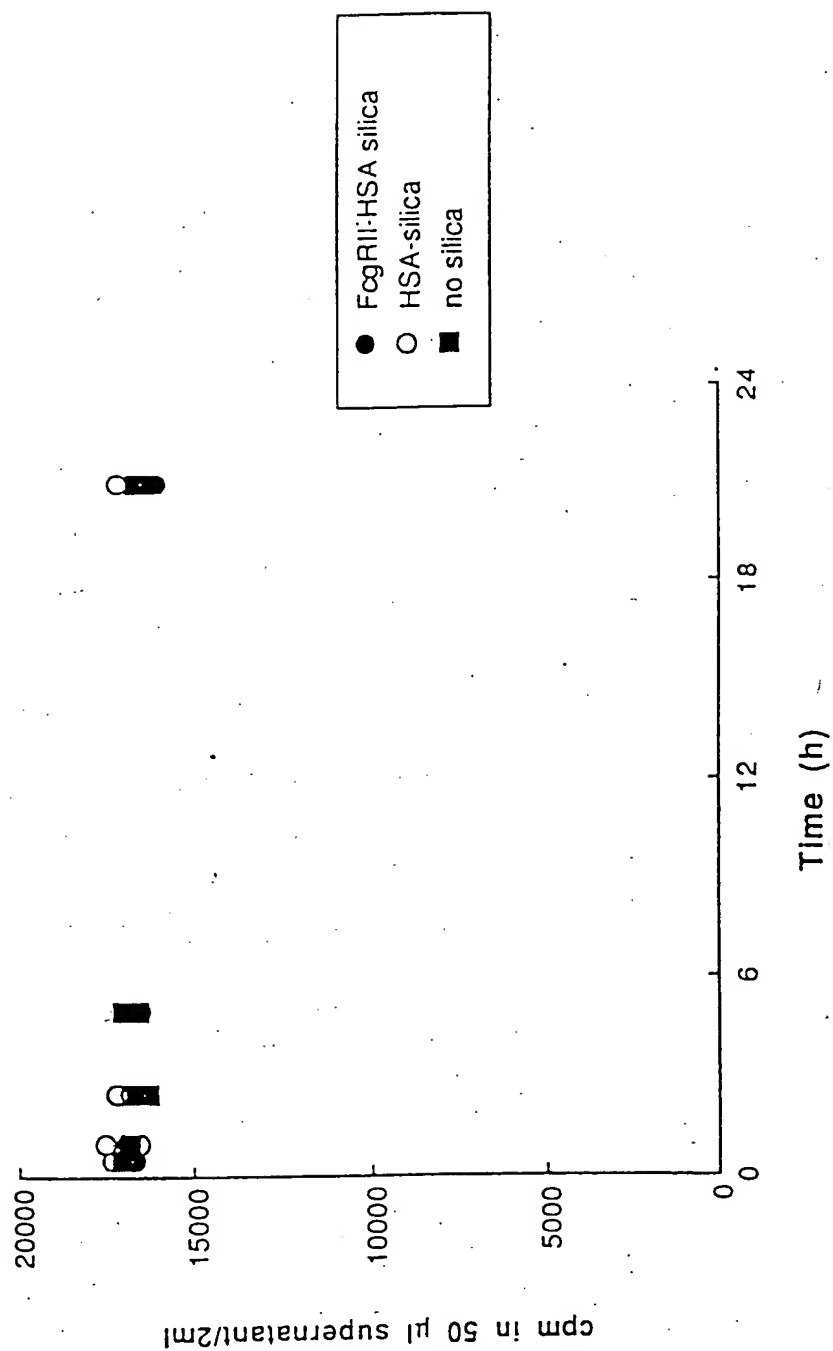


FIGURE 17

Functional soluble Fc γ RII detected binding to hagg using the MoAb 8.2

Titration of rsFc γ RII from various sources

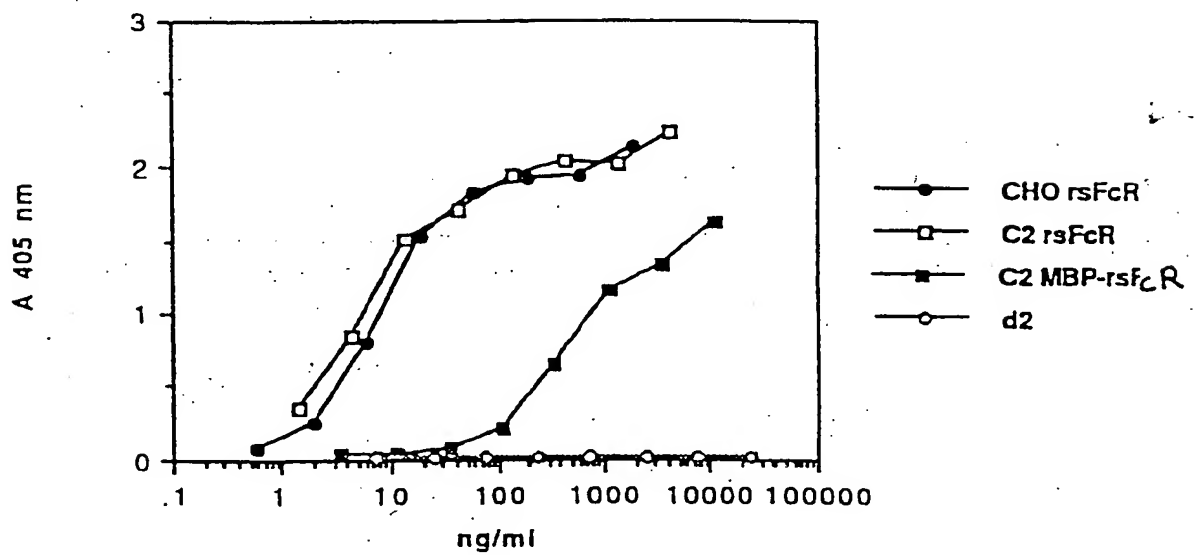


FIGURE 18

Human serum containing rheumatoid factors, but not normal human sera, inhibits the binding of HRP conjugated to rsHSA-FcγRII to hagg.

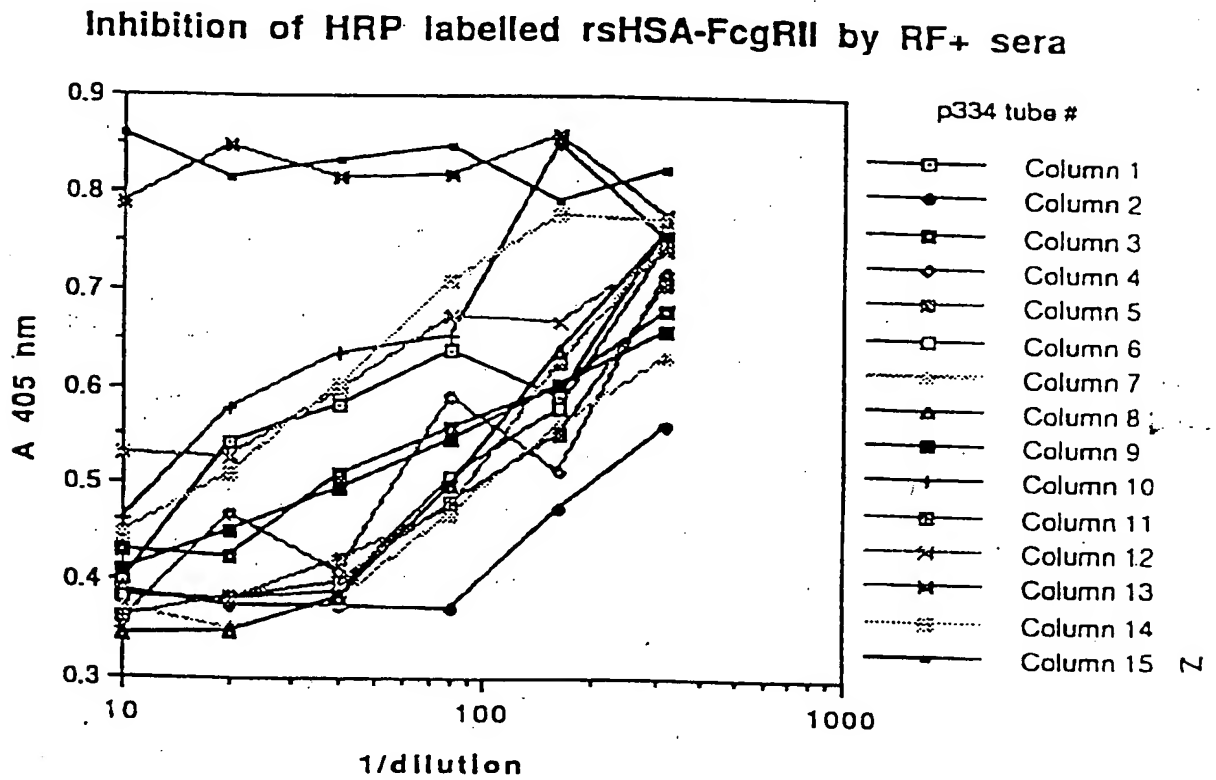


FIGURE 19

Peptoid name	A 405 nm (X 1000)	Peptoid name	A 405 nm (X 1000)
TC,1	308.5	NB,1	578.5
AD,1	317	BD,1	580
DC,1	319	OA,1	582.5
SC,1	319	DJ,1	586
AC,1	320	LG,1	586.5
RC,1	323.5	VF,1	586.5
NC,1	329.5	OG,1	587
UC,1	329.5	DS,1	587
LC,1	330.5	IF,1	588
FC,1	332.5	RA,1	588
JC,1	335	DL,1	589.5
HC,1	343	QB,1	591
QC,1	345.5	QF,1	592
GC,1	346.5	EU,1	592
CU,1	356	JE,1	592
MC,1	357	DQ,1	592.5
EC,1	358	AF,1	594
DG,1	359.5	SB,1	594
IC,1	363	HA,1	594.5
CF,1	363	IG,1	596
CG,1	364	HB,1	596.5
CV,1	364	DO,1	596.5
VC,1	364	RB,1	597
		Background	304
		Maximum	619